

FIGURE 1

loci	allelic designat ion	size (bp)	loci	allelic designat ion	size (bp)	loci	allelic designat ion n	size (bp)	loci	allelic designa tion n	size (bp)
TH01	4	150	D8	7	157	D18	8	266	FGA (LMW)	16.1	173
	5	154		8	161		6	270		17	176
	9	158		6	165		10	274		18	180
	7	162		10	169		11	278		19	184
	8	166		II	173		12	282		20	188
	6	170		12	177		13	286		21	192
	9.3	173		13	181		14	290		22	196
	10	174		14	185		15	294		23	200
	11	178		15	189		16	298		24	204
	13.3	189		16	193		17	302		25	208
D2.1	53	203		1.7	197		18	306		26	212
	54	205		18	201		19	310		27	216
	56	209		19	205		20	314		28	220
	57	211	VWA	10	122		21	318		29	224
	59	215		11	126		22	322		30	228
	61	219		12	130		23	326		30.2	230
	63	223		13	134		24	330		31.2	234
	65	227		14	138		25	334		32.2	238
	29	231		15	142		26	338		33.2	242
11								·			







89	233	16	146		27	342	34.2	246
70	237	17	150	AMELO	X	105	42.2	278
72	241	18	154		Y	111	42.3	282
74	245	19	158				44.2	286
75	247	20	162				45.2	290
77	251	21	166				46.2	294
79	255						47.2	298
81	259						48.2	302
							50.2	310
-								



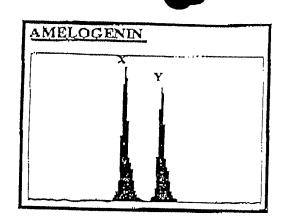


Fig 2a

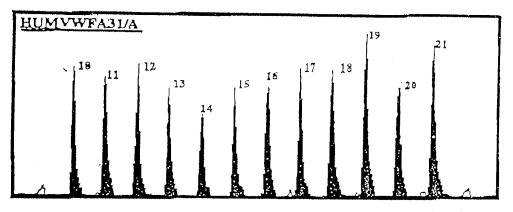


Fig 2b

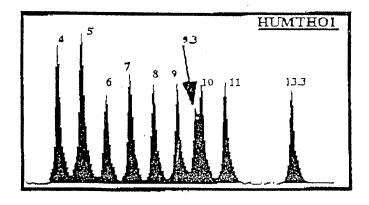


Fig 2c

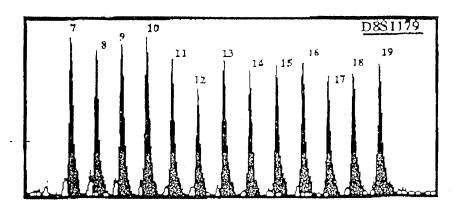
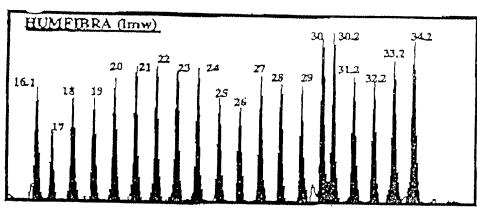


Fig 2d



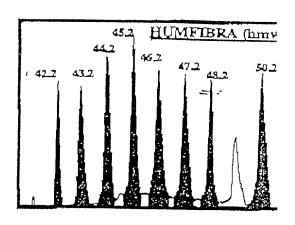
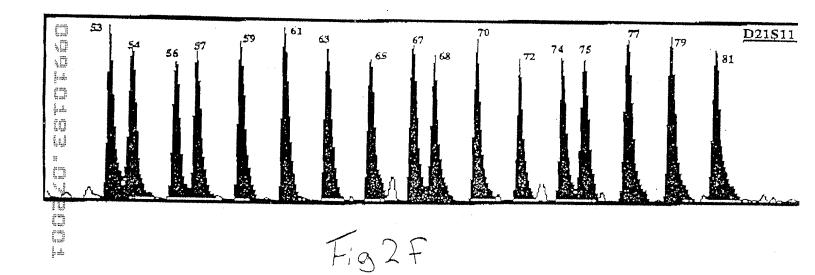


Fig2e



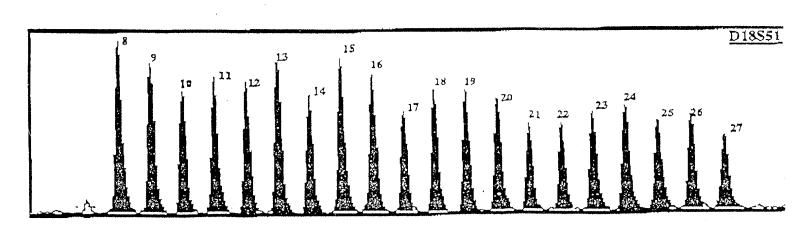


Fig 2g





HUMVWAF31/A sequences

- 10 TCTA TCTG TCTA (TCTG)4 (TCTA)3
- 12 TCTA (TCTG)₄ (TCTA)₇

Fig 3a

13 (TCTA)₂ (TCTG)₄ (TCTA)₅ TCCA (TCTA)₅ (TCCA)₂ T (Note also that the 13 allele has a typical 3' flanking sequence (highlighted). The usual sequence is TCCA TCTA T.)

HUMTHO1 sequences

13.3 (TCAT), CAT (TCAT), TCGT TCAT.

Fig3b

D8\$1179 sequences

7 (TCTA)₈;

[q (TCTA)₂ TCTG(TCTA)₁₆;

Fig3c

Fig 3d

HUMFIBRA(FGA) Repeat Sequences

- 16.1 (TTTC)₃ TTTT TTCT (CTTT)₅ T (CTTT)₅ CTCC (TTCC)₂
- 27 (TTTC)₃ TTTT TTCT (CTTT)₁₅ CCTT (CTTT)₅ CTCC (TTCC)₂.
- 30 (TTTC)₃ TTTT TTCT (CTTT)₁₆ CCTT (CTTT)₅ CTCC (TTCC)₂.
- 31.2 (TTTC), TTTT TT (CTTT)15 (CTTC)3 (CTTT)3 CTCC (TTCC)4.
- 32.2 (TTTC)₄ TTTT TT (CTTT)₁₆ (CTTC)₅ (CTTT)₃ CTCC (TTCC)₄
- 33.2 (TTTC)4 TTTT TT (CTTT)17 (CTTC)3 (CTTT)3 CTCC (TTCC)4
- 42.2 (TTTC)4 TTTT TT (CTTT)8 (CTGT)4 (CTTT)13 (CTTC)4 (CTTT)3 CTCC (TTCC) 4
- 43.2 (TTTC)₄ TFTT TT (CTTT)₈ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC (TTCC)₄
- 44.2 (TTTC)₄ TTTT TT (CTTT)₁₁ (CTGT)₅ (CTTT)₁₄ (CTTC)₅ (CTTT)₅ CTCC (TTCC)₄
- 45.2 (TTTC)₄ TTTT TT (CTTT)₁₀ (CTGT)₅ (CTTT)₁₃ (CTTC)₄ (CTTT)₃ CTCC (TTCC)₄
 - 47.2 (TTTC), TTTT TT (CTTT), (CTGT), (CTTT), (CTTC), (CTTT), CTCC (TTCC),
 - 48.2 (TTTC), TTTT TT (CTTT), (CTGT), (CTTT), (CTTC), (CTTC), (CTTC), (CTTC),





D21S11 alleles

- 53 (TCTA)₄ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)
 6 TCGTCT
- 54 (TCTA)₅ (TCTG)₆ (TCTA)₅ TCA (TCTA)₂ TCCATA (TCTA)₅ TCGTCT
- 56 (TCTA)₅ (TCTG)₆ (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₀ TCGTCT
- 57 (TCTA)₄ (TCTG)₆ (TCTA)₅ TA (TCTA)₅ TCA (TCTA)₂ TCCATA (TCTA)₈ TCGTCT
- 59 (TCTA)₅ (TCTG)₅ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)
- 61 (TCTA)₄ (TCTG)₆ (TCTA)₅ TA (TCTA)₅ TCA (TCTA)₂ TCCATA (TCTA)
 20 TCGTCT
- 63 (TCTA)₄ (TCTG)₆ (TCTA)₅ TA (TCTA)₅ TCA (TCTA)₂ TCCATA (TCTA)
 21 TCGTCT
- 65 (TCTA)6 (TCTG)5 (TCTA)3 TA (TCTA)3 TCA (TCTA)2 TCCATA (TCTA)

 "TCGTCT"
- 67 (TCTA)5 (TCTG)6 (TCTA)5 TA (TCTA)5 TCA (TCTA)2 TCCATA (TCTA)2 TCGTCT
- 68 (TCTA); (TCTG); (TCTA); TA (TCTA); TCA (TCTA); TCCATA (TCTA); TA TCTA TCGTCT.
- 70 (TCTA)₅ (TCTG)₆ (TCTA)₅ TA (TCTA)₅ TCA (TCTA)₂ TCCATA (TCTA)₂₂ TA TCTA TCGTCT
- 72 (TCTA)₅ (TCTG)₆ (TCTA)₃ TA (TCTA)₃ TCA (TCTA)₂ TCCATA (TCTA)₁₃ TA TCTA TCGTCT
- 74 (TCTA)₅ (TCTG)₆ (TCTA)₅ TA (TCTA)₅ TCA (TCTA)₂ TCCATA (TCTA)₄ TATCTA TCGTCT
- 75 (TCTA), (TCTG), (TCTA), TA (TCTA), TCA (TCTA), TCCATA (TCTA), TCGTCT
- 77 (TCTA) 11 (TCTG)5 (TCTA)5 TA (TCTA)5 TCA (TCTA)2 TCCATA (TCTA)22 TCGTCT
- 79 (TCTA)₁₁ (TCTG)₅ (TCTA)₅ TA (TCTA)₅ TCA (TCTA)₁₅ TCGTCT
- 81 (TCTA) $_5$ (TCTG) $_5$ (TCTA) $_5$ TA (TCTA) $_5$ TCA (TCTA) $_2$ TCCATA (TCTA) $_2$ TCGTCT

D18S51 sequences

8 (AGAA)8

Fig3F

Fig3e